GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2006, 17:12:50 ; Search time 19405 Seconds
                                          (without alignments)
                                          19849.129 Million cell updates/sec

Title: US-10-804-772-1
Perfect score: 6888
Sequence: 1 atgtgggtattatatttgttg..........cctagttcaggccaaagctt 6888

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

Database :   EST:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result   Query
   No.   Score Match Length DB ID   Description

	No.	Score	Match	Length	DB	ID	Description
c	1	744.4	10.8	900	13	CL514078	CL514078 SAIL_882_
	2	727	10.6	1605	6	CNS0A4TW	BX824287 Arabidops
	3	695	10.1	1797	6	CNS0A70Q	BX822540 Arabidops

	4	541.4	7.9	543	11	B77695	B77695 T28K14TF TA
	5	534.2	7.8	563	14	BX292216	BX292216 Arabidops
	6	526.6	7.6	1038	4	BX839458	BX839458 BX839458
	7	485.4	7.0	651	7	AV824772	AV824772 AV824772
c	8	474	6.9	845	14	DU985218	DU985218 KBrH1076J
c	9	426.2	6.2	937	13	CL493476	CL493476 SAIL_580_
	10	401.2	5.8	457	14	CR397647	CR397647 Arabidops
	11	385.6	5.6	1397	14	AJ859443	AJ859443 Brassica
	12	372.8	5.4	460	14	CR397648	CR397648 Arabidops
c	13	359	5.2	434	3	BP606549	BP606549 BP606549
	14	355.6	5.2	375	12	CC797957	CC797957 SALK_1456
c	15	343.6	5.0	423	7	AV787618	AV787618 AV787618
c	16	337	4.9	951	13	CL516966	CL516966 SAIL_98_C
	17	333.4	4.8	698	5	CD814113	CD814113 BN15.022A
c	18	320	4.6	424	3	BP603351	BP603351 BP603351
c	19	320	4.6	446	3	BP612187	BP612187 BP612187
c	20	309.2	4.5	342	14	BX533508	BX533508 Arabidops
c	21	305.6	4.4	363	3	BP622314	BP622314 BP622314
	22	296	4.3	965	4	BX839894	BX839894 BX839894
c	23	291.8	4.2	908	13	CL516967	CL516967 SAIL_98_C
c	24	283	4.1	416	3	BP565879	BP565879 BP565879
c	25	283	4.1	417	3	BP563350	BP563350 BP563350
c	26	283	4.1	433	3	BP564785	BP564785 BP564785
c	27	272	3.9	414	3	BP575355	BP575355 BP575355
	28	270	3.9	364	3	BP803469	BP803469 BP803469
c	29	269.2	3.9	404	3	BP580791	BP580791 BP580791
c	30	266.6	3.9	273	11	BZ287389	BZ287389 SALK_0207
c	31	263	3.8	875	13	CL469983	CL469983 SAIL_136_
c	32	255.8	3.7	370	3	BP567237	BP567237 BP567237
	33	252.6	3.7	360	3	BP803450	BP803450 BP803450
c	34	251	3.6	442	3	BP577809	BP577809 BP577809
	35	234.2	3.4	923	13	CL502551	CL502551 SAIL_713_
c	36	209	3.0	788	11	BZ483015	BZ483015 BONNO30TR
	37	205.6	3.0	552	10	DT014799	DT014799 VVI092G03
	38	205.4	3.0	647	3	BU887383	BU887383 R058F09 P
	39	203.8	3.0	659	8	CX182444	CX182444 D12_45-46
	40	203.8	3.0	806	10	DT503533	DT503533 WS0136.BR
	41	203.4	3.0	943	10	DT568185	DT568185 EST107882
	42	202.8	2.9	753	10	DV134569	DV134569 CV03108B2
	43	201.2	2.9	602	10	DT013384	DT013384 VVH050E10
	44	201.2	2.9	645	10	DT014183	DT014183 VVH009D08
	45	199	2.9	490	10	DT009234	DT009234 VVH034D03

ALIGNMENTS

RESULT 1
CL514078/c
LOCUS   CL514078   900 bp   DNA   linear   GSS 01-APR-2004
DEFINITION SAIL_882_F07.v2 SAIL Collection Arabidopsis thaliana genomic clone
            SAIL_882_F07.v2, genomic survey sequence.
ACCESSION   CL514078
VERSION   CL514078.1 GI:46011398
KEYWORDS   GSS.
SOURCE   Arabidopsis thaliana (thale cress)
  ORGANISM Arabidopsis thaliana

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2006, 16:30:37 ; Search time 24949 Seconds
                                         (without alignments)
                                        17654.809 Million cell updates/sec

Title: US-10-804-772-1
Perfect score: 6888
Sequence: 1 atgtgggtattatattgttg..........cctagttcaggccaaagctt 6888

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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                 13: gb_in:*
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                 15: gb_ba:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                              SUMMARIES

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   No.   Score   Match Length DB   ID   Description
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     2   4818   69.9   4818   4   AF044216   AF044216 Arabidops

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        5   722.4   10.5    1542    4   AY090266         AY090266 Arabidops
        6    669     9.7    1035    2   CS258452         CS258452 Sequence
        7   384.6    5.6 121254    4   CT033768         CT033768 Medicago
        8   381.2    5.5 134939    4   AC147964         AC147964 Medicago
    c   9    377     5.5 130026   12   AC174298          AC174298 Medicago
    c  10   331.4    4.8  96298   12   AP007781          AP007781 Lotus cor
       11   205.2    3.0   1777    4   AB231155         AB231155 Zinnia el
       12   187.6    2.7 110000    4   AP008209_066     Continuation (67 o
       13   187.6    2.7 110000    4   AP008209_067     Continuation (68 o
       14   187.6    2.7 127946    4   AC104473         AC104473 Oryza sat
       15   176.8    2.6    191    7   AL844732         AL844732 Arabidops
    c  16   140.4    2.0   8056    2   AX599046          AX599046 Sequence
       17   136.4    2.0   8056    2   AX599046         AX599046 Sequence
       18   135.6    2.0   6508    2   AR566958         AR566958 Sequence
       19   135.6    2.0 250029   13   AE014839          AE014839 Plasmodiu
       20   135      2.0 349751   13   PFMAL4P3          AL035476 Plasmodiu
       21   134      1.9 100269    4   ATF18O22         AL163817 Arabidops
       22   133.2    1.9 104992   12   AC005504         AC005504 Plasmodiu
       23   133.2    1.9 169546   12   AC004157         AC004157 Plasmodiu
    c  24   133.2    1.9 250421   13   AE014849          AE014849 Plasmodiu
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    c  31   130.4    1.9 254050   13   PFA929358         AL929358 Plasmodiu
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       33   128.6    1.9 172816    5   AC093899         AC093899 Homo sapi
       34   128      1.9 106142    4   AC025417         AC025417 Genomic s
       35   127.8    1.9  86826   13   PFMAL3P5          AL034556 Plasmodiu
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       40   124.4    1.8   4601   13   DMU11584         U11584 Drosophila
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                              ALIGNMENTS

RESULT 1
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LOCUS   ATT3A5   84196 bp   DNA   linear   PLN 16-APR-2005
DEFINITION   Arabidopsis thaliana DNA chromosome 3, BAC clone T3A5.
ACCESSION   AL132979
VERSION   AL132979.2 GI:6782244
KEYWORDS   .
SOURCE   Arabidopsis thaliana (thale cress)
  ORGANISM   Arabidopsis thaliana

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OM nucleic - nucleic search, using sw model

Run on: August 1, 2006, 05:51:05 ; Search time 804 Seconds
                                           (without alignments)
                                           16030.096 Million cell updates/sec

Title: US-10-804-772-1
Perfect score: 6888
Sequence: 1 atgtgggtattatattgttg..........cctagttcaggccaaagctt 6888

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

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      3   94.6   1.4   1181 3 US-09-464-535-35   Sequence 35, Appl
      4   92.8   1.3   4937 2 US-08-622-166A-3   Sequence 3, Appli
      5   88.2   1.3   453 3 US-09-464-535-11   Sequence 11, Appl
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  c   7   84   1.2 18773 3 US-09-949-016-14164   Sequence 14164, A

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c  13   80.8   1.2  191569   3   US-09-949-016-15940     Sequence 15940, A
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ALIGNMENTS

RESULT 1
US-09-502-426B-1
; Sequence 1, Application US/09502426B
; Patent No. 6987025
; GENERAL INFORMATION:
; APPLICANT: Azpiroz, Ricardo
; APPLICANT: Choe, Sunghwa
; APPLICANT: Feldmann, Kenneth A.
; TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 11696-070001
; CURRENT APPLICATION NUMBER: US/09/502,426B
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/119,657
; PRIOR FILING DATE: 1999-02-11

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OM nucleic - nucleic search, using sw model

Run on: August 1, 2006, 05:56:48 ; Search time 5055 Seconds
                                          (without alignments)
                                          16743.270 Million cell updates/sec

Title: US-10-804-772-1
Perfect score: 6888
Sequence: 1 atgtgggtattatattgttg..........cctagttcaggccaaagctt 6888

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                                   SUMMARIES
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Result   Query
   No.   Score Match Length DB ID   Description
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	2	3379	49.1	3379	16	US-11-112-824-19	Sequence 19, Appl
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	28	87.6	1.3	1419	3	US-09-938-842A-619	Sequence 619, App
	29	87.6	1.3	1649	16	US-11-172-740-2328	Sequence 2328, Ap
	30	87.6	1.3	1682	16	US-11-208-308-1	Sequence 1, Appli
C	31	87.4	1.3	158001	8	US-10-211-179-11	GENERAL INFORMATI
	32	87	1.3	173602	15	US-11-121-086-25	Sequence 25, Appl
C	33	86.8	1.3	755	6	US-10-027-632-128109	Sequence 128109,
C	34	86.8	1.3	755	7	US-10-027-632-128109	Sequence 128109,
C	35	86.4	1.3	38678	10	US-10-893-315-136	Sequence 136, App
C	36	86.4	1.3	38684	10	US-10-893-315-154	Sequence 154, App
	37	86.4	1.3	158001	8	US-10-211-179-11	GENERAL INFORMATI
	38	84.6	1.2	9810	7	US-10-311-455-400	Sequence 400, App
	39	84.2	1.2	26772	10	US-10-995-561-13313	Sequence 13313, A
	40	84.2	1.2	54946	10	US-10-995-561-13479	Sequence 13479, A
C	41	83.8	1.2	8170	7	US-10-240-453-131	Sequence 131, App
	42	82.8	1.2	6131	7	US-10-311-455-863	Sequence 863, App
	43	82.6	1.2	9810	7	US-10-311-455-399	Sequence 399, App
C	44	82.6	1.2	15732	6	US-10-239-676-95	Sequence 95, Appl
C	45	82.6	1.2	15732	7	US-10-240-453-107	Sequence 107, App

ALIGNMENTS

RESULT 1
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